

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/591,540  
Source: IFWP  
Date Processed by STIC: 9/18/06

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IFWP

**RAW SEQUENCE LISTING**

PATENT APPLICATION: US/10/591,540

DATE: 09/18/2006

TIME: 15:20:32

Input Set : E:\SEQUENCE LISTING PCT.EP.2005.002450 (65084.23).txt  
 Output Set: N:\CRF4\09182006\J591540.raw

3 <110> APPLICANT: Frohberg, Claus  
 4 Koetting, Oliver  
 5 Ritte, Gerhard  
 6 Steup, Martin  
 8 <120> TITLE OF INVENTION: Plants with reduced activity of multiple starch  
 phosphorylating enzymes  
 10 <130> FILE REFERENCE: 65084.000023  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/591,540  
 13 <141> CURRENT FILING DATE: 2006-09-01  
 15 <150> PRIOR APPLICATION NUMBER: EP04090088.8  
 16 <151> PRIOR FILING DATE: 2004-03-05  
 18 <150> PRIOR APPLICATION NUMBER: EP04090121.7  
 19 <151> PRIOR FILING DATE: 2004-03-29  
 21 <150> PRIOR APPLICATION NUMBER: US60/550,022  
 22 <151> PRIOR FILING DATE: 2004-03-05  
 24 <150> PRIOR APPLICATION NUMBER: EP04090203.3  
 25 <151> PRIOR FILING DATE: 2004-05-21  
 27 <150> PRIOR APPLICATION NUMBER: EP04090484.9  
 28 <151> PRIOR FILING DATE: 2004-12-09  
 30 <160> NUMBER OF SEQ ID NOS: 31  
 32 <170> SOFTWARE: PatentIn version 3.1  
 34 <210> SEQ ID NO: 1  
 35 <211> LENGTH: 3591  
 36 <212> TYPE: DNA  
 37 <213> ORGANISM: Arabidopsis thaliana  
 39 <220> FEATURE:  
 40 <221> NAME/KEY: CDS  
 41 <222> LOCATION: (1)...(3591)  
 42 <223> OTHER INFORMATION:  
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 47 Met Glu Ser Ile Gly Ser His Cys Cys Ser Ser Pro Phe Thr Phe Ile  
 48 1 5 10 15  
 50 act aga aac tca tca tca ctt cct aga ctc gtt aac atc act cac 96  
 51 Thr Arg Asn Ser Ser Ser Leu Pro Arg Leu Val Asn Ile Thr His  
 52 20 25 30  
 54 aga gtt aat ctc agc cac caa tct cac cga ctc aga aac tcc aat tct 144  
 55 Arg Val Asn Leu Ser His Gln Ser His Arg Leu Arg Asn Ser Asn Ser  
 56 35 40 45  
 58 cgt ctc act tgc act gct act tct tct tcc acc att gag gaa caa cgg 192  
 59 Arg Leu Thr Cys Thr Ala Thr Ser Ser Thr Ile Glu Glu Gln Arg  
 60 50 55 60  
 62 aag aag aaa gat gga tca gga acg aaa gtg agg ttg aat gtg agg tta 240  
 63 Lys Lys Lys Asp Gly Thr Lys Val Arg Leu Asn Val Arg Leu

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66	gat	cat	caa	gtt	aat	ttt	ggc	gac	cat	gtg	gct	atg	ttt	gga	tca	gct	288
67	Asp	His	Gln	Val	Asn	Phe	Gly	Asp	His	Val	Ala	Met	Phe	Gly	Ser	Ala	
68																95	
70	aaa	gag	att	ggc	tca	tgg	aaa	aag	aaa	tcg	cct	ttg	aat	tgg	agt	gag	336
71	Lys	Glu	Ile	Gly	Ser	Trp	Lys	Lys	Ser	Pro	Leu	Asn	Trp	Ser	Glu		
72																110	
74	aat	gga	tgg	gtt	tgt	gag	ttg	gaa	ctt	gac	ggc	gtt	cag	ttg	gag	384	
75	Asn	Gly	Trp	Val	Cys	Glu	Leu	Glu	Leu	Asp	Gly	Gly	Gln	Val	Leu	Glu	
76																125	
78	tat	aag	ttt	gtc	att	gtt	aag	aat	gat	ggc	tca	ctt	tca	tgg	gaa	tct	432
79	Tyr	Lys	Phe	Val	Ile	Val	Lys	Asn	Asp	Gly	Ser	Leu	Ser	Trp	Glu	Ser	
80																140	
82	ggc	gtt	aat	cgt	gtc	ctt	aag	gtt	cca	aat	tct	ggg	aat	ttt	tct	gtt	480
83	Gly	Asp	Asn	Arg	Val	Leu	Lys	Val	Pro	Asn	Ser	Gly	Asn	Phe	Ser	Val	
84	145															160	
86	gtt	tgt	cat	tgg	gtt	gat	act	aga	gaa	acc	ctt	gat	ttg	cct	cag	gag	528
87	Val	Cys	His	Trp	Asp	Ala	Thr	Arg	Glu	Thr	Leu	Asp	Leu	Pro	Gln	Glu	
88																175	
90	gtt	ggc	aat	gat	gtt	gat	gtt	ggc	cat	gag	agg	gtt	aat				576
91	Val	Gly	Asn	Asp	Asp	Asp	Val	Gly	Asp	Gly	Gly	His	Glu	Arg	Asp	Asn	
92																190	
94	cat	gat	gtt	ggc	gtt	gat	aga	gtt	gtt	gga	agt	gaa	aat	ggc	cag	624	
95	His	Asp	Val	Gly	Asp	Asp	Arg	Val	Val	Gly	Ser	Glu	Asn	Gly	Ala	Gln	
96																205	
98	ctt	cag	aag	agt	aca	ttt	ggc	ggg	caa	tgg	caa	ggc	aaa	gat	gcg	tcc	672
99	Leu	Gln	Lys	Ser	Thr	Leu	Gly	Gly	Gln	Trp	Gln	Gly	Lys	Asp	Ala	Ser	
100																220	
102	ttt	atg	cgt	tct	aat	gat	cat	ggc	aac	aga	gaa	gtt	ggc	aat	tgg	720	
103	Phe	Met	Arg	Ser	Asn	Asp	His	Gly	Asn	Arg	Glu	Val	Gly	Arg	Asn	Trp	
104	195															240	
106	gat	act	agt	ggc	ctt	gaa	ggc	aca	gct	ctt	aag	atg	gtt	gag	ggc	gtt	768
107	Asp	Thr	Ser	Gly	Leu	Glu	Gly	Thr	Ala	Leu	Lys	Met	Val	Glu	Gly	Asp	
108																255	
110	cgc	aac	tct	aag	aac	tgg	tgg	aga	aag	ctt	gaa	atg	gtt	gta	cgc	gag	816
111	Arg	Asn	Ser	Lys	Asn	Trp	Trp	Arg	Lys	Leu	Glu	Met	Val	Arg	Glu	Val	
112																270	
114	ata	gtt	ggg	agt	gtt	gag	agg	gag	gaa	cga	ttt	aag	gcg	ctc	ata	tac	864
115	Ile	Val	Gly	Ser	Val	Glu	Arg	Glu	Glu	Arg	Leu	Lys	Ala	Leu	Ile	Tyr	
116																285	
118	tct	gca	att	tat	ttt	aag	tgg	ata	aac	aca	ggc	cag	att	cct	tgt	ttt	912
119	Ser	Ala	Ile	Tyr	Leu	Lys	Trp	Ile	Asn	Thr	Gly	Gln	Ile	Pro	Cys	Phe	
120																300	
122	gaa	gat	ggg	cat	cac	cgt	cca	aac	agg	cat	gcc	gag	att	tcc	aga		960
123	Glu	Asp	Gly	Gly	His	His	Arg	Pro	Asn	Arg	His	Ala	Glu	Ile	Ser	Arg	
124	305															320	
126	ctt	ata	ttc	cgt	gag	ttt	gag	cac	att	tgc	agt	aag	aaa	gat	gct	act	1008
127	Leu	Ile	Phe	Arg	Glu	Leu	Glu	His	Ile	Cys	Ser	Lys	Lys	Asp	Ala	Thr	
128																335	

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130 cca gag gaa gtg ctt gtt gct cggtt	aaa atc cat ccgtt	tgt tta cct tct	1056
131 Pro Glu Glu Val Leu Val Ala Arg Lys Ile His Pro Cys Leu Pro Ser			
132 340	345	350	
134 ttc aaa gca gag ttt act gca gct gtc cct cta act ccgtt	att agg gac		1104
135 Phe Lys Ala Glu Phe Thr Ala Ala Val Pro Leu Thr Arg Ile Arg Asp			
136 355	360	365	
138 ata gcc cat ccgtt	aat gat att cct cat gat ctc aag caa gaa atc aag		1152
139 Ile Ala His Arg Asn Asp Ile Pro His Asp Leu Lys Gln Glu Ile Lys			
140 370	375	380	
142 cat acg ata caa aat aag ctt cac ccgtt	aat gct ggctt	cca gaa gat cta	1200
143 His Thr Ile Gln Asn Lys Leu His Arg Asn Ala Gly Pro Glu Asp Leu			
144 385	390	395	400
146 att gca aca gaa gca atg ctt caa cga att acc gag acc cca gga aaa			1248
147 Ile Ala Thr Glu Ala Met Leu Gln Arg Ile Thr Glu Thr Pro Gly Lys			
148 405	410	415	
150 tat agt gga gac ttt gtg gag cag ttt aaa ata ttc cat aat gag ctt			1296
151 Tyr Ser Gly Asp Phe Val Glu Gln Phe Lys Ile Phe His Asn Glu Leu			
152 420	425	430	
154 aaa gat ttgtt aat gct gga agt ctc act gaa cag ctt gat tctatg			1344
155 Lys Asp Phe Phe Asn Ala Gly Ser Leu Thr Glu Gln Leu Asp Ser Met			
156 435	440	445	
158 aaa att tct atg gat gat aga ggt ctt tct gcg ctc aat ttg ttt ttt			1392
159 Lys Ile Ser Met Asp Asp Arg Gly Leu Ser Ala Leu Asn Leu Phe Phe			
160 450	455	460	
162 gaa tgt aaa aag cgc ctt gac aca tca gga aat tca agc aat gtt ttg			1440
163 Glu Cys Lys Lys Arg Leu Asp Thr Ser Gly Glu Ser Ser Asn Val Leu			
164 465	470	475	480
166 gag ttg att aaa acc atg cat tct cta gct tct tta aga gaa aca att			1488
167 Glu Leu Ile Lys Thr Met His Ser Leu Ala Ser Leu Arg Glu Thr Ile			
168 485	490	495	
170 ata aag gaa ctt aat agc ggc ttg cga aat gat gct cct gat act gcc			1536
171 Ile Lys Glu Leu Asn Ser Gly Leu Arg Asn Asp Ala Pro Asp Thr Ala			
172 500	505	510	
174 att gca atg cgc cag aag tgg cgc ctt tgg gag atc ggc ctc gag gac			1584
175 Ile Ala Met Arg Gln Lys Trp Arg Leu Cys Glu Ile Gly Leu Glu Asp			
176 515	520	525	
178 tac ttt ttt gtt cta cta agc aga ttc ctc aat gct ctt gaa act atg			1632
179 Tyr Phe Phe Val Leu Leu Ser Arg Phe Leu Asn Ala Leu Glu Thr Met			
180 530	535	540	
182 gga gga gct gat caa ctg gca aaa gat gtg gga tca aga aac gtt gcc			1680
183 Gly Gly Ala Asp Gln Leu Ala Lys Asp Val Gly Ser Arg Asn Val Ala			
184 545	550	555	560
186 tca tgg aat gat cca cta gat gct ttg gtt ggt gtt cac caa gta			1728
187 Ser Trp Asn Asp Pro Leu Asp Ala Leu Val Leu Gly Val His Gln Val			
188 565	570	575	
190 ggt cta tct ggt tgg aag caa gaa gaa tgt tta gcc att gga aat gaa			1776
191 Gly Leu Ser Gly Trp Lys Gln Glu Glu Cys Leu Ala Ile Gly Asn Glu			
192 580	585	590	
194 ctc ctt gct tgg cga gaa agg gac cta ctt gaa aaa gaa ggg gaa gag			1824

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196				595		600						605					
198	gat	gga	aaa	aca	att	tgg	gcc	atg	agg	ctg	aaa	gca	act	ctt	gat	cga	1872
199	Asp	Gly	Lys	Thr	Ile	Trp	Ala	Met	Arg	Leu	Lys	Ala	Thr	Leu	Asp	Arg	
200				610				615				620					
202	gca	cgc	aga	tta	aca	gca	gaa	tat	tct	gat	ttg	ctt	caa	ata	ttt		1920
203	Ala	Arg	Arg	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	Leu	Leu	Gln	Ile	Phe		
204	625				630				635				640				
206	cct	cct	aat	gtg	gag	att	tta	gga	aaa	gct	cta	gga	att	cca	gag	aat	1968
207	Pro	Pro	Asn	Val	Glu	Ile	Leu	Gly	Lys	Ala	Leu	Gly	Ile	Pro	Glu	Asn	
208					645				650			655					
210	agt	gtc	aag	acc	tat	aca	gaa	gca	gag	att	cgt	gct	gga	att	att	ttc	2016
211	Ser	Val	Lys	Thr	Tyr	Thr	Glu	Ala	Glu	Ile	Arg	Ala	Gly	Ile	Ile	Phe	
212					660				665			670					
214	cag	atc	tca	aag	ctc	tgc	act	gtt	ctt	cta	aaa	gct	gta	aga	aat	tca	2064
215	Gln	Ile	Ser	Lys	Leu	Cys	Thr	Val	Leu	Leu	Lys	Ala	Val	Arg	Asn	Ser	
216		675				680			685								
218	ctt	ggg	tct	gag	ggc	tgg	gat	gtc	gtt	gta	cct	gga	tcg	acg	tct	ggg	2112
219	Leu	Gly	Ser	Glu	Gly	Tyr	Asp	Val	Val	Val	Pro	Gly	Ser	Thr	Ser	Gly	
220		690			695				700								
222	aca	tta	gtt	cag	gtt	gag	agc	att	gtt	ccg	gga	tca	ttg	cca	gca	act	2160
223	Thr	Leu	Val	Gln	Val	Glu	Ser	Ile	Val	Pro	Gly	Ser	Leu	Pro	Ala	Thr	
224	705				710				715			720					
226	tct	ggg	ggt	cct	att	att	ctc	ttg	gtc	aat	aaa	gct	gat	ggc	gat	gaa	2208
227	Ser	Gly	Gly	Pro	Ile	Ile	Leu	Leu	Val	Asn	Lys	Ala	Asp	Gly	Asp	Glu	
228					725				730			735					
230	gag	gta	agt	gct	aat	ggg	aac	ata	gct	gga	gtc	atg	ctt	ctg	cag		2256
231	Glu	Val	Ser	Ala	Ala	Asn	Gly	Asn	Ile	Ala	Gly	Val	Met	Leu	Leu	Gln	
232		740			745				750								
234	gag	ctg	cct	cac	ttg	tct	cac	ctt	ggc	gtt	aga	gcg	cg	cag	gag	aaa	2304
235	Glu	Leu	Pro	His	Leu	Ser	His	Leu	Gly	Val	Arg	Ala	Arg	Gln	Glu	Lys	
236		755			760			765									
238	att	gtc	ttt	gtg	aca	tgt	gat	gat	gat	gac	aag	gtt	gct	gat	ata	cga	2352
239	Ile	Val	Phe	Val	Thr	Cys	Asp	Asp	Asp	Asp	Lys	Val	Ala	Asp	Ile	Arg	
240		770			775			780									
242	cga	ctt	gtg	gga	aaa	ttt	gtg	agg	ttg	gaa	gca	tct	cca	agt	cat	gtg	2400
243	Arg	Leu	Val	Gly	Lys	Phe	Val	Arg	Leu	Glu	Ala	Ser	Pro	Ser	His	Val	
244	785				790			795			800						
246	aat	ctg	ata	ctt	tca	act	gag	gg	agg	agt	cgc	act	tcc	aaa	tcc	agt	2448
247	Asn	Leu	Ile	Leu	Ser	Thr	Glu	Gly	Arg	Ser	Arg	Thr	Ser	Lys	Ser	Ser	
248					805			810			815						
250	gcg	acc	aaa	aaa	acg	gat	aag	aac	agc	tta	tct	aag	aaa	aaa	aca	gat	2496
251	Ala	Thr	Lys	Lys	Thr	Asp	Lys	Asn	Ser	Leu	Ser	Lys	Lys	Thr	Asp		
252		820			825			830									
254	aag	aag	agc	tta	tct	atc	gat	gat	gaa	gaa	tca	aag	cct	gg	tca		2544
255	Lys	Lys	Ser	Leu	Ser	Ile	Asp	Asp	Glu	Glu	Ser	Lys	Pro	Gly	Ser	Ser	
256		835			840			845									
258	tct	tcc	aat	agc	ctc	ctt	tac	tct	tcc	aag	gat	atc	cct	agt	gga	gga	2592
259	Ser	Ser	Asn	Ser	Leu	Leu	Tyr	Ser	Ser	Lys	Asp	Ile	Pro	Ser	Gly	Gly	

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260	850	855	860	
262	atc ata gca ctt gct gat gca gat gta cca act tct ggt tca aaa tct			2640
263	Ile Ile Ala Leu Ala Asp Ala Asp Val Pro Thr Ser Gly Ser Lys Ser			
264	865	870	875	880
266	gct gca tgt ggt ctt ctt gca tct tta gca gaa gcc tct agt aaa gtg			2688
267	Ala Ala Cys Gly Leu Leu Ala Ser Leu Ala Glu Ala Ser Ser Lys Val			
268	885	890	895	
270	cac agc gaa cac gga gtt ccg gca tca ttt aag gtt cca act gga gtt			2736
271	His Ser Glu His Gly Val Pro Ala Ser Phe Lys Val Pro Thr Gly Val			
272	900	905	910	
274	gtc ata cct ttt gga tcg atg gaa tta gct tta aag caa aat aat tcg			2784
275	Val Ile Pro Phe Gly Ser Met Glu Leu Ala Leu Lys Gln Asn Asn Ser			
276	915	920	925	
278	gaa gaa aag ttt gcg tct ttg cta gaa aaa cta gaa acc gcc aga cct			2832
279	Glu Glu Lys Phe Ala Ser Leu Leu Glu Lys Leu Glu Thr Ala Arg Pro			
280	930	935	940	
282	gag ggt ggt gag cta gac gac ata tgt gac cag atc cat gaa gtg atg			2880
283	Glu Gly Gly Glu Leu Asp Asp Ile Cys Asp Gln Ile His Glu Val Met			
284	945	950	955	960
286	aaa acg ttg caa gtg cct aaa gaa aca atc aac agc ata agc aaa gcg			2928
287	Lys Thr Leu Gln Val Pro Lys Glu Thr Ile Asn Ser Ile Ser Lys Ala			
288	965	970	975	
290	ttt ctc aaa gat gct cgt ctc att gtt cgt tca agt gct aac gtc gag			2976
291	Phe Leu Lys Asp Ala Arg Leu Ile Val Arg Ser Ser Ala Asn Val Glu			
292	980	985	990	
294	gac tta gcc gga atg tca gct gca gga ctc tat gaa tca atc cct aac			3024
295	Asp Leu Ala Gly Met Ser Ala Ala Gly Leu Tyr Glu Ser Ile Pro Asn			
296	995	1000	1005	
298	gtg agt ccc tcg gat cct ttg gtg ttt tca gat tcg gtt tgc caa			3069
299	Val Ser Pro Ser Asp Pro Leu Val Phe Ser Asp Ser Val Cys Gln			
300	1010	1015	1020	
302	gtt tgg gct tct ctc tac aca aga aga gct gtt cta agc cgt aga			3114
303	Val Trp Ala Ser Leu Tyr Thr Arg Arg Ala Val Leu Ser Arg Arg			
304	1025	1030	1035	
306	gct gct ggt gtc tct caa aga gaa gct tca atg gct gtt ctc gtt			3159
307	Ala Ala Gly Val Ser Gln Arg Glu Ala Ser Met Ala Val Leu Val			
308	1040	1045	1050	
310	caa gaa atg ctt tcg ccg gac tta tca ttc gtt ctg cac aca gtg			3204
311	Gln Glu Met Leu Ser Pro Asp Leu Ser Phe Val Leu His Thr Val			
312	1055	1060	1065	
314	agt cca gct gat ccg gac agt aac ctt gtg gaa gcc gag atc gct			3249
315	Ser Pro Ala Asp Pro Asp Ser Asn Leu Val Glu Ala Glu Ile Ala			
316	1070	1075	1080	
318	cct ggt tta ggt gag act tta gct tca gga aca aga gga aca cca			3294
319	Pro Gly Leu Gly Glu Thr Leu Ala Ser Gly Thr Arg Gly Thr Pro			
320	1085	1090	1095	
322	tgg aga ctc gct tcg ggt aag ctc gac ggg att gta caa acc tta			3339
323	Trp Arg Leu Ala Ser Gly Lys Leu Asp Gly Ile Val Gln Thr Leu			
324	1100	1105	1110	

**VERIFICATION SUMMARY**

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number

L:45 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:42

L:673 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:670

L:1364 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:1361